



Patent
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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re the Application of:

Neil H. Bander

Serial No.: 09/929,665

Filed: July 20, 1999

(Continuation of S.N. 09/357,704 (242/024))

For: TREATMENT AND DIAGNOSIS OF PROSTATE CANCER

Group Art Unit: 1642

Examiner: Not yet assigned

TRANSMITTAL OF SUBSTITUTE DRAWINGS UNDER 37 CFR 1.84

Commissioner for Patents
Washington, D.C. 20231

Sir:

In response to a Notice to File Corrected Application Papers, Applicant transmits herewith substitute drawings (11 sheets) in compliance with the requirements of 37 CFR 1.84. These drawings are deemed formal drawings and are identical to those previously submitted in the parent U.S. Patent Application Serial No. 09/357,704.

No fee is deemed necessary in the filing of the substitute drawings. However, should a fee be deemed necessary, the Commissioner is authorized and requested to charge any amounts due on

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(37 C.F.R. §1.8a)

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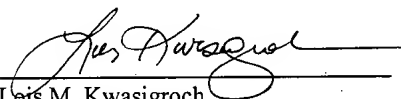
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account of the present submission to the Deposit Account of the undersigned attorneys, which is:
Deposit Account No. 12-2475.

Respectfully submitted,
LYON & LYON LLP

Dated: October 25, 2001

By: _____


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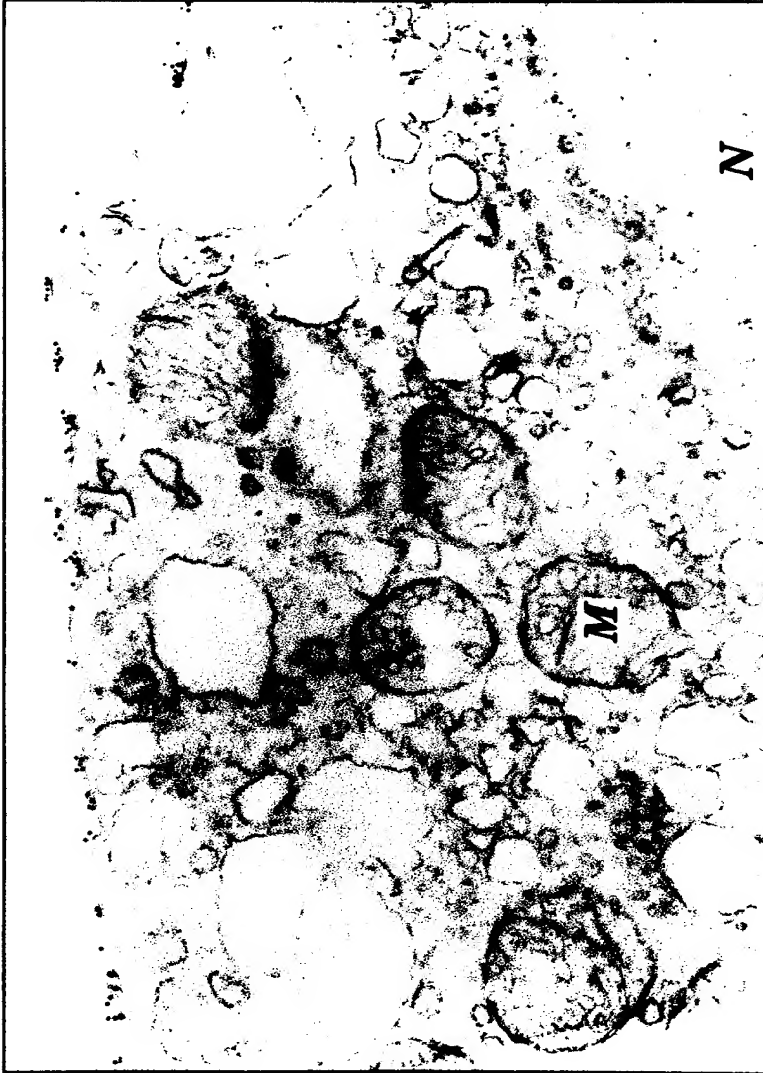


FIG. 1

09929665-120701

02/11

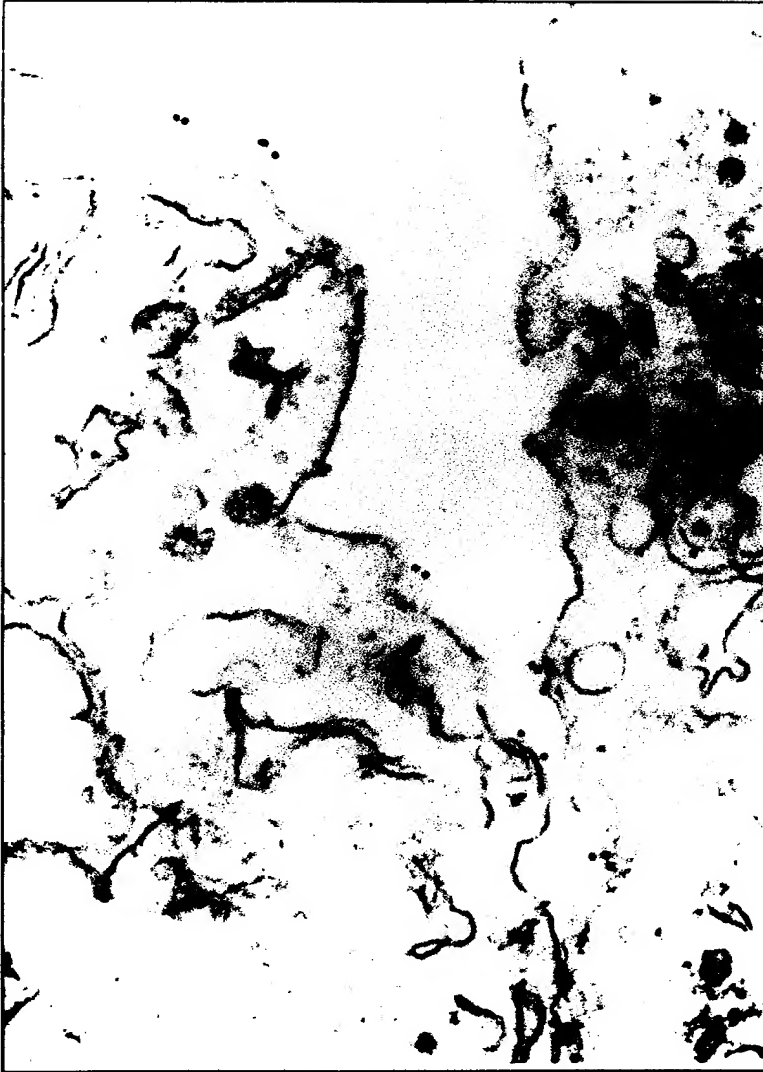


FIG. 2

104021" 59962650

03/11

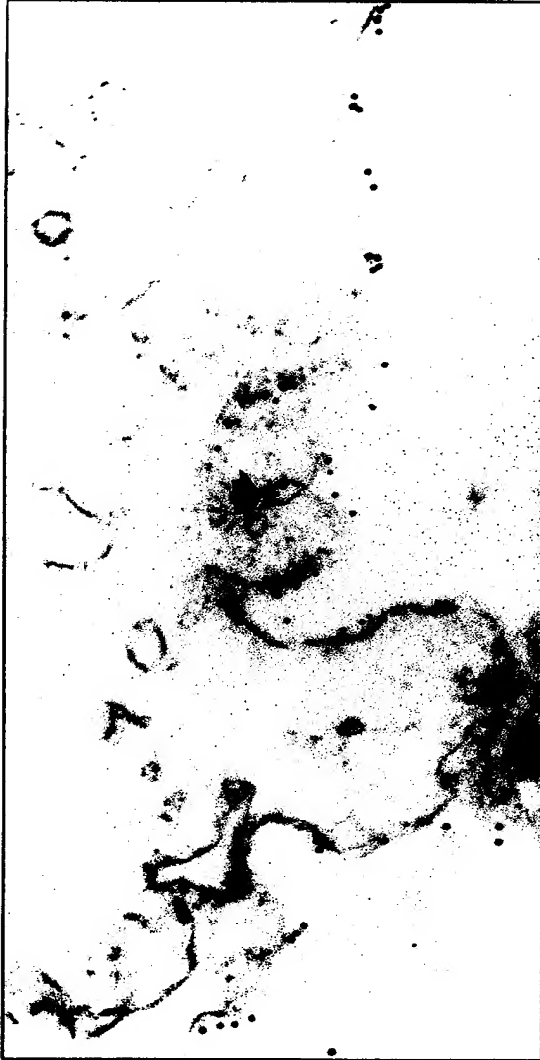


FIG. 3

09929665.120701

04/11

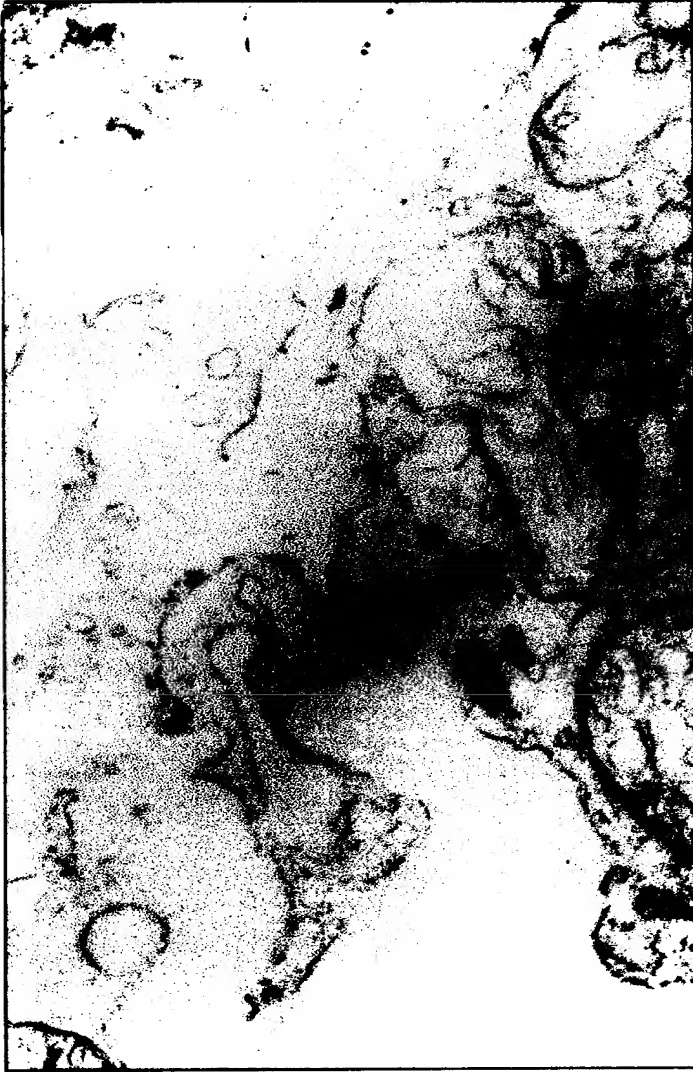


FIG. 4

FD/02T" 59962660

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FIG. 5

T0702T"59062660

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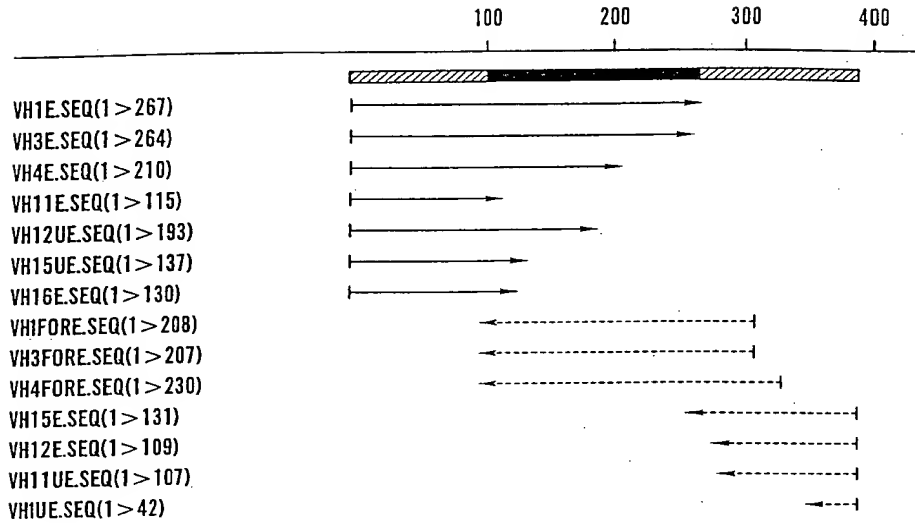


FIG. 6

07/11

ENZYMES: ALL 74 ENZYMES (NO FILTER)

SETTINGS: LINEAR, CERTAIN SITES ONLY, STANDARD GENETIC CODE

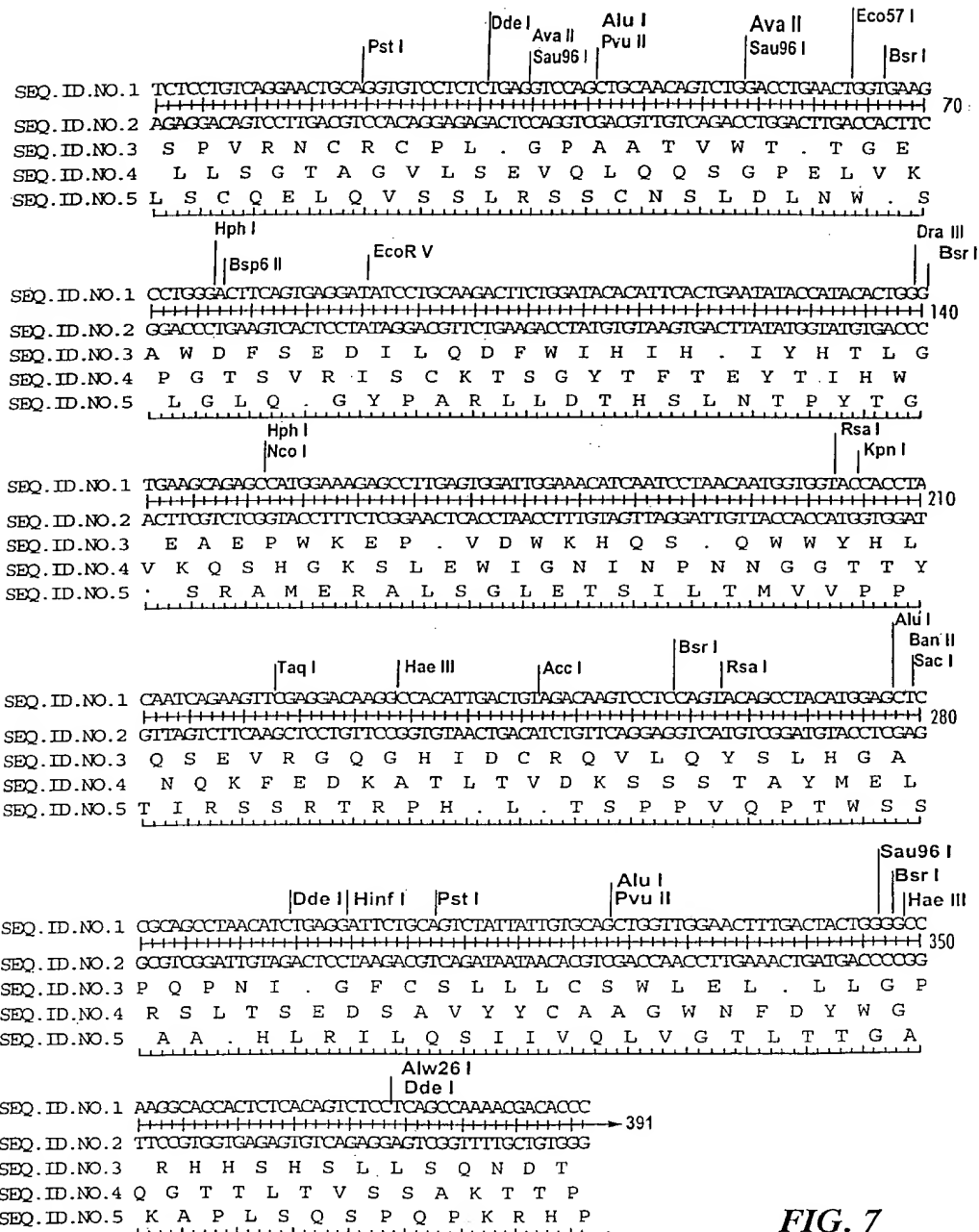


FIG. 7

08/11

LIPMAN-PEARSON PROTEIN ALIGNMENT
 KTUPLE: 2; GAP PENALTY: 4; GAP LENGTH PENALTY: 12

SEQ1(1>115)	SEQ2(1>125)	SIMILARITY	GAP	GAP	CONSENSUS
J591VH.PRO	MUVHIIA.PRO	INDEX	NUMBER	LENGTH	LENGTH
(1>115)	(1>125)	75.6	2	10	125

EVQLQQSGPELVKPGTISVRISCKTSGYTFTEXTI-HWVKQSHGKSLEWIGNINENNGGIT
 EVQLQQSGPELVKPG:SV:ISCK:SGYTFT:Y : :WVKQS.GKSLEWIG:INP.NGGT:
 EVQLQQSGPELVKPGASVKISCKASGYTFIDYYMNNWVKQSPGKSLEWIGDINPNNGGTS
 YNQKFEDKATLTIVDKSSSTAYMELRSLTSEDSAVYYCAAG-----WNFDYWGGITT
 YNQKF.:KATLTIVDKSSSTAYM:L.SLTSEDSAVYYCA G ..FDYWGGITT
 YNQKFKGKATLTIVDKSSSTAYMQLSSLTSEDSAVYYCARGYYSSSYMAYYAFDYWGQGIT

10 20 30 40 50
 60 70 80 90 100 110
 70 80 90 100 110 120

LIVSS

:IVSS

VIVSS

FIG. 8

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#6

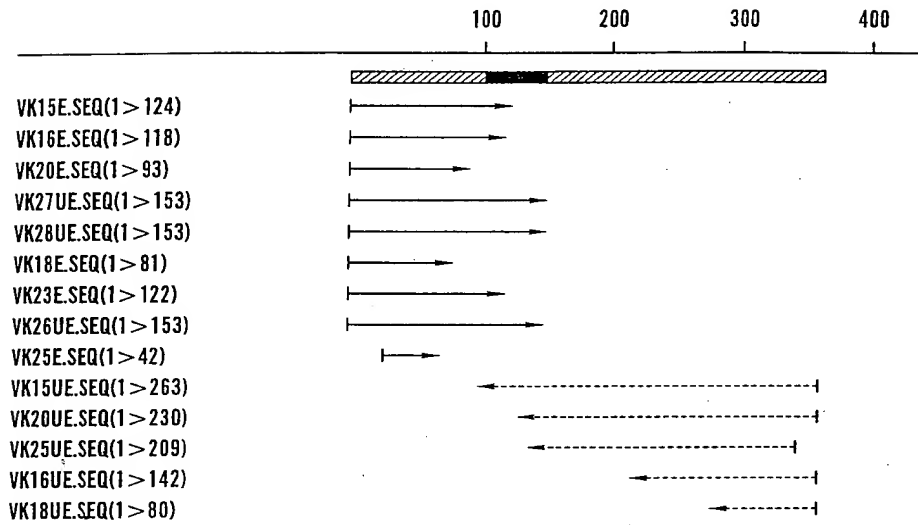


FIG. 9

10/11

ENZYMES: ALL 74 ENZYMES (NO FILTER):
SETTINGS: LINEAR, CERTAIN SITES ONLY, STANDARD GENETIC CODE

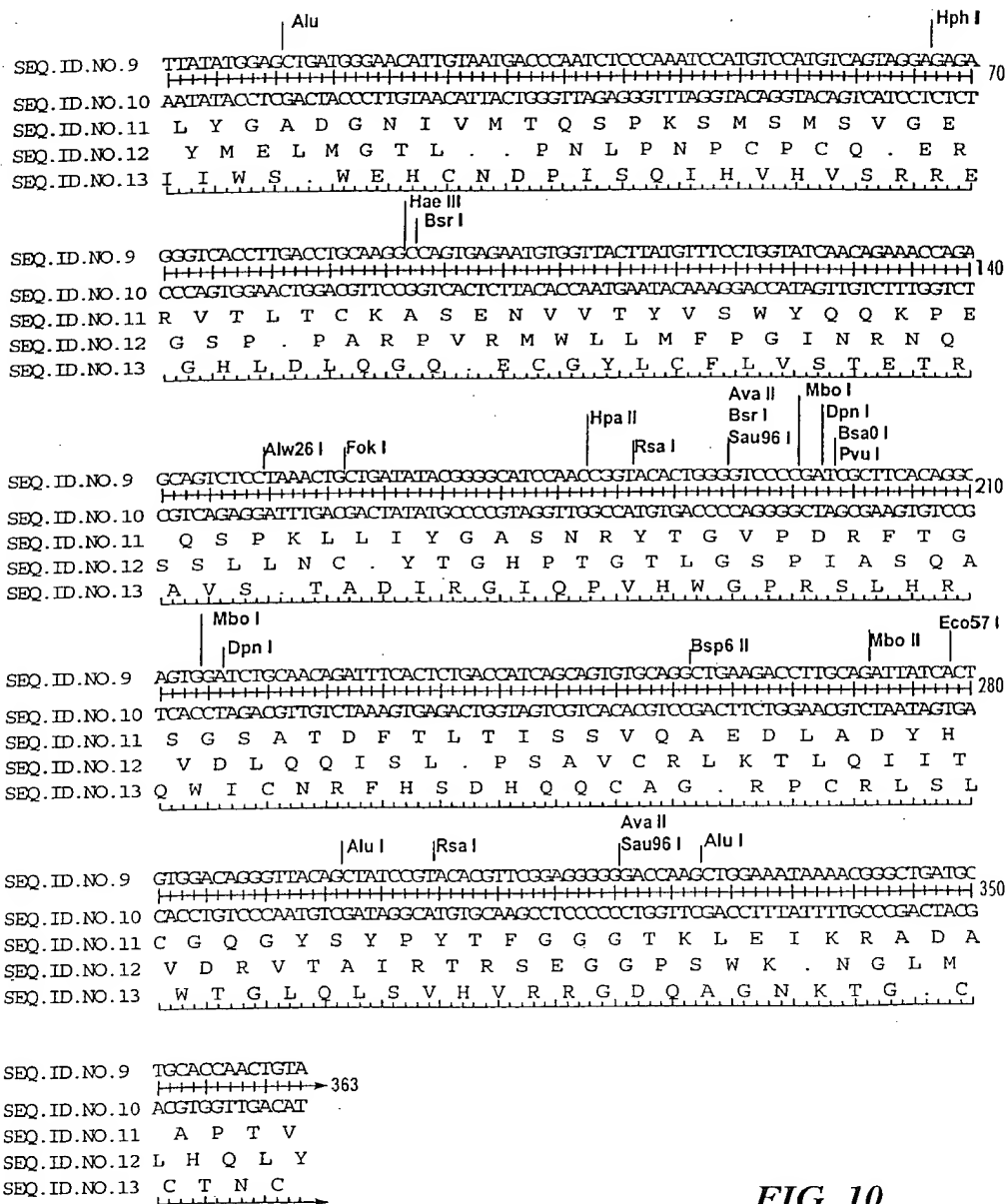


FIG. 10

09929665-120701

11/11

LIPMAN-PEARSON PROTEIN ALIGNMENT

KTUPLE: 2; GAP PENALTY: 4; GAP LENGTH PENALTY: 12

SEQ1(1>107)	SEQ2(1>111)	SIMILARITY	GAP	GAP	CONSENSUS
J591VK.PRO	MUVKV.PRO	INDEX	NUMBER	LENGTH	LENGTH
(1>107)	(1>109)	60.4	2	2	109

10 20 30 40 50
 NIVMTQSPKSMMSVGERVILTCKAS-ENVVTYVSWYQOKPEQSPKLLIYGASNRYTGVP
 :I MTQSP.S:S S:G:RVT:TC:AS ::: .Y::WYQOKP. SPKLLIY AS. :GVP
 DIQMIQSPSSLSASLGDRVTITCRASQDDISNYLNWYQOKPGGSPKLLIYYASRLHSGVP
 10 20 30 40 50 60
 60 70 80 90 100
 DRFTGSGSATDFTLTISVQAEDLADYHCGQGY-SY-PYTFGGGKLEIK
 .RF:GSGS:TD::LTIS:::ED:A.Y C QG : P TFGGGKLEIK
 SRFSGSGSGIDYSLTISNLEQEDIATYFQQGNILPRTFGGGKLEIK
 70 80 90 100

FIG. 11